```
   16   503.5   28.1    556  2  Q16GN5_AEDAE            Q16gn5 aedes aegyp
   17   502.5   28.1    556  2  Q0IG10_AEDAE            Q0ig10 aedes aegyp
   18     485   27.1    458  2  Q8MQ76_CAEEL            Q8mq76 caenorhabdi
   19     485   27.1    560  2  Q29BP0_DROPS            Q29bp0 drosophila
   20     453   25.3    551  2  Q8IMY3_DROME            Q8imy3 drosophila
   21     453   25.3    561  2  Q9VCJ4_DROME            Q9vcj4 drosophila
   22     453   25.3    573  2  Q4V4F5_DROME            Q4v4f5 drosophila
   23     453   25.3    577  2  Q4V4J1_DROME            Q4v4j1 drosophila
   24     444   24.8    561  2  O16581_CAEEL            O16581 caenorhabdi
   25   441.5   24.7    523  2  O16580_CAEEL            O16580 caenorhabdi
   26     441   24.6    524  2  Q611J0_CAEBR            Q611j0 caenorhabdi
   27   440.5   24.6    495  2  Q611J5_CAEBR            Q611j5 caenorhabdi
   28   432.5   24.1    572  2  Q9AT27_PHYIN            Q9at27 phytophthor
   29     421   23.5    424  2  Q4V4A3_DROME            Q4v4a3 drosophila
   30     409   22.8    423  2  Q7PXX9_ANOGA            Q7pxx9 anopheles g
   31   392.5   21.9    445  2  A4XMF5_CALSA            A4xmf5 caldicellul
   32   376.5   21.0    468  2  Q2AI75_9FIRM            Q2ai75 halothermot
   33   369.5   20.6    495  2  A3J0N5_9FLAO            A3j0n5 flavobacter
   34     369   20.6    443  2  Q8R5Q0_THETN            Q8r5q0 thermoanaer
   35   345.5   19.3    494  2  A6EGQ6_9SPHI            A6egq6 pedobacter
   36   340.5   19.0    445  2  Q1FLM6_9CLOT            Q1flm6 clostridium
   37   340.5   19.0    548  2  Q8PBP2_XANCP            Q8pbp2 xanthomonas
   38     331   18.5    499  2  Q1VR53_9FLAO            Q1vr53 psychroflex
   39   330.5   18.5    474  2  A2TWU2_9FLAO            A2twu2 polaribacte
   40     328   18.3    489  2  Q3BWD0_XANC5            Q3bwd0 xanthomonas
   41     324   18.1    458  2  Q8PN97_XANAC            Q8pn97 xanthomonas
   42   321.5   18.0    439  2  Q4URV7_XANC8            Q4urv7 xanthomonas
   43   318.5   17.8    236  2  Q66IW2_XENLA            Q66iw2 xenopus lae
   44   318.5   17.8    487  2  A5FJM1_CYTJO            A5fjm1 flavobacter
   45   313.5   17.5    490  2  Q1YUE9_9GAMM            Q1yue9 gamma prote


                                 ALIGNMENTS


RESULT 1
GLCM_HUMAN
ID   GLCM_HUMAN   ←      Reviewed;         536 AA.
AC   P04062; Q16545; Q4VX22; Q6I9R6; Q9UMJ8;
DT   01-NOV-1986, integrated into UniProtKB/Swiss-Prot.
DT   09-NOV-2004, sequence version 3.
DT   21-AUG-2007, entry version 105.
DE   Glucosylceramidase precursor (EC 3.2.1.45) (Beta-glucocerebrosidase)
DE   (Acid beta-glucosidase) (D-glucosyl-N-acylsphingosine glucohydrolase)
DE   (Alglucerase) (Imiglucerase).
GN   Name=GBA; Synonyms=GC, GLUC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT).
RC   TISSUE=Placenta;
RX   MEDLINE=86042651; PubMed=3864160;
RA   Sorge J., West C., Westwood B., Beutler E.;
RT   "Molecular cloning and nucleotide sequence of human glucocerebrosidase
RT   cDNA.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:7289-7293(1985).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM SHORT).
RC   TISSUE=Hepatoma;
RX   MEDLINE=86085859; PubMed=3001061;
RA   Tsuji S., Choudary P.V., Martin B.M., Winfield S., Barranger J.A.,
RA   Ginns E.I.;
RT   "Nucleotide sequence of cDNA containing the complete coding sequence
RT   for human lysosomal glucocerebrosidase.";
RL   J. Biol. Chem. 261:50-53(1986).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   TISSUE=Liver;
RX   MEDLINE=89122038; PubMed=2914709; DOI=10.1016/0888-7543(89)90319-4;
RA   Horowitz M., Wilder S., Horowitz Z., Reiner O., Gelbart T.,
RA   Beutler E.;
RT   "The human glucocerebrosidase gene and pseudogene: structure and
RT   evolution.";
RL   Genomics 4:87-96(1989).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC   TISSUE=Liver;
RX   MEDLINE=92241881; PubMed=1572652; DOI=10.1016/0888-7543(92)90311-F;
RA   Beutler E., West C., Gelbart T.;
RT   "Polymorphisms in the human glucocerebrosidase gene.";
RL   Genomics 12:795-800(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS LONG AND 3), VARIANTS GD ARG-223;
RP   GLY-230; PRO-235; ARG-241; ILE-252 AND ARG-364, AND VARIANTS GLY-310
RP   AND HIS-368.
RX   MEDLINE=94124033; PubMed=8294033; DOI=10.1016/0378-1119(93)90497-Q;
RA   Imai K., Nakamura M., Yamada M., Asano A., Yokoyama S., Tsuji S.,
RA   Ginns E.I.;
RT   "A novel transcript from a pseudogene for human glucocerebrosidase in
RT   non-Gaucher disease cells.";
RL   Gene 136:365-368(1993).
RN   [6]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=97474796; PubMed=9331372;
RA   Winfield S.L., Tayebi N., Martin B.M., Ginns E.I., Sidransky E.;
RT   "Identification of three additional genes contiguous to the
RT   glucocerebrosidase locus on chromosome 1q21: implications for Gaucher
RT   disease.";
RL   Genome Res. 7:1020-1026(1997).
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=16710414; DOI=10.1038/nature04727;
RA   Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D.,
RA   Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A.,
RA   Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F.,
RA   McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C.,
RA   Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P.,
RA   Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K.,
RA   Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G.,
RA   Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D.,
RA   Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G.,
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RA   Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J.,
RA   Deadman R., Dunn M., Earthrowl M., Ellington A.G., Errington H.,
RA   Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L.,
RA   Ghori M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J.,
RA   Grafham D.V., Griffiths C., Griffiths-Jones S., Grocock R.,
RA   Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D.,
RA   Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G.,
RA   Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M.,
RA   Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J.,
RA   Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M.,
RA   Loveland J., Lovell J., Lush M.J., Lyne R., Martin S.,
RA   Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S.,
RA   Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N.,
RA   Oliver K., Palmeiri A., Palmer S.A., Parker A., Patel D., Pearce A.V.,
RA   Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J.,
RA   Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E.,
RA   Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C.,
RA   Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z.,
RA   Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E.,
RA   Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A.,
RA   Vaudin M., Sulston J.E., Durbin R.M., Hubbard T., Wooster R.,
RA   Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V.,
RA   Beck S., Rogers J., Bentley D.R.;
RT   "The DNA sequence and biological annotation of human chromosome 1.";
RL   Nature 441:315-321(2006).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RC   TISSUE=Placenta;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA
RT   project: the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA] OF 1-11.
RX   MEDLINE=88195776; PubMed=3359914;
RA   Reiner O., Wigderson M., Horowitz M.;
RT   "Structural analysis of the human glucocerebrosidase genes.";
RL   DNA 7:107-116(1988).
RN   [10]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-45.
RX   MEDLINE=88074307; PubMed=3687939;
RA   Sorge J.A., West C., Kuhl W., Treger L., Beutler E.;
RT   "The human glucocerebrosidase gene has two functional ATG initiator
RT   codons.";
RL   Am. J. Hum. Genet. 41:1016-1024(1987).
RN   [11]
RP   PROTEIN SEQUENCE OF 40-44.
RC   TISSUE=Placenta;
RA   Martin B.M., Murray G.J., Coligan J.E., Raum M., Brady R.O.,
RA   Barranger J.A.;
RT   "Sturctural studies of human placental glucocerebrosidase.";
RL   Fed. Proc. 43:1869-1869(1984).
RN   [12]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 403-416.
RX   MEDLINE=85022513; PubMed=6091633;
RA   Ginns E.I., Choudary P.V., Martin B.M., Winfield S., Stubblefield B.,
RA   Mayor J., Merkle-Lehman D., Murray G.J., Bowers L.A., Barranger J.A.;
RT   "Isolation of cDNA clones for human beta-glucocerebrosidase using the
RT   lambda gt11 expression system.";
RL   Biochem. Biophys. Res. Commun. 123:574-580(1984).
RN   [13]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 409-462, AND VARIANT GD SER-409.
RC   TISSUE=Skin;
RX   MEDLINE=88176943; PubMed=3353383;
RA   Tsuji S., Martin B.M., Barranger J.A., Stubblefield B.K.,
RA   LaMarca M.E., Ginns E.I.;
RT   "Genetic heterogeneity in type 1 Gaucher disease: multiple genotypes
RT   in Ashkenazic and non-Ashkenazic individuals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:2349-2352(1988).
RN   [14]
RP   PROTEIN SEQUENCE OF 469-520.
RC   TISSUE=Placenta;
RX   MEDLINE=86149363; PubMed=3456607;
RA   Dinur T., Osiecki K.M., Legler G., Gatt S., Desnick R.J.,
RA   Grabowski G.A.;
RT   "Human acid beta-glucosidase: isolation and amino acid sequence of a
RT   peptide containing the catalytic site.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:1660-1664(1986).
RN   [15]
RP   MASS SPECTROMETRY, MUTAGENESIS OF GLU-379, AND ACTIVE SITE.
RX   PubMed=7908905;
RA   Miao S., McCarter J.D., Grace M.E., Grabowski G.A., Aebersold R.,
RA   Withers S.G.;
RT   "Identification of Glu340 as the active-site nucleophile in human
RT   glucocerebrosidase by use of electrospray tandem mass spectrometry.";
RL   J. Biol. Chem. 269:10975-10978(1994).
RN   [16]
RP   INTERACTION WITH SAPOSIN-C AND MEMBRANES CONTAINING ANIONIC
RP   PHOSPHOLIPIDS.
RX   PubMed=10781797; DOI=10.1016/S0014-5793(00)01417-4;
RA   Salvioli R., Tatti M., Ciaffoni F., Vaccaro A.M.;
RT   "Further studies on the reconstitution of glucosylceramidase activity
RT   by Sap C and anionic phospholipids.";
RL   FEBS Lett. 472:17-21(2000).
RN   [17]
RP   GLYCOSYLATION AT ASN-98; ASN-185 AND ASN-309.
RX   MEDLINE=22660472; PubMed=12754519; DOI=10.1038/nbt827;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
RN   [18]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 40-536, GLYCOSYLATION AT
RP   ASN-58, AND DISULFIDE BONDS.
RX   PubMed=12792654; DOI=10.1038/sj.embor.embor873;
RA   Dvir H., Harel M., McCarthy A.A., Toker L., Silman I., Futerman A.H.,
RA   Sussman J.L.;
RT   "X-ray structure of human acid-beta-glucosidase, the defective enzyme
RT   in Gaucher disease.";
RL   EMBO Rep. 4:704-709(2003).
RN   [19]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 40-536 IN COMPLEX WITH
RP   SYNTHETIC INHIBITOR, AND ACTIVE SITE.
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RX   PubMed=15817452; DOI=10.1074/jbc.M502799200;
RA   Premkumar L., Sawkar A.R., Boldin-Adamsky S., Toker L., Silman I.,
RA   Kelly J.W., Futerman A.H., Sussman J.L.;
RT   "X-ray structure of human acid-beta-glucosidase covalently bound to
RT   conduritol-B-epoxide. Implications for Gaucher disease.";
RL   J. Biol. Chem. 280:23815-23819(2005).
RN   [20]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 40-536, CHARACTERIZATION OF
RP   GD VARIANTS SER-55; GLN-87; ASN-118; GLN-159; LEU-161; VAL-162;

  Query Match            94.2%;  Score 1687;  DB 1;  Length 536;
  Best Local Similarity   67.0%;  Pred. No. 8.6e-137;
  Matches  333;  Conservative    1;  Mismatches    1;  Indels  162;  Gaps    1;

Qy          1 ARPCIPKSFGYSSVVCVCNATYCDSFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ARPCIPKSFGYSSVVCVCNATYCDSFDPPTFPALGTFSRYESTRSGRRMELSMGPIQANH 99

Qy         61 TGTGLLLTLQPEQKFQKVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEG------- 113
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 TGTGLLLTLQPEQKFQKVKGFGGAMTDAAALNILALSPPAQNLLLKSYFSEEGIGYNIIR 159

Qy        114 ------------------------------------------------------------ 113

Db        160 VPMASCDFSIRTYTYADTPDDFQLHNFSLPEEDTKLKIPLIHRALQLAQRPVSLLASPWT 219

Qy        114 ------------------------------------------------------------ 113

Db        220 SPTWLKTNGAVNGKGSLKGQPGDIYHQTWARYFVKFLDAYAEHKLQFWAVTAENEPSAGL 279

Qy        114 -----------------------------------VRLLMLNDQRLLLPHWAKVVLTDPE 138
                                                 ||||||:||||||||||||||||||
Db        280 LSGYPFQCLGFTPEHQRDFIARDLGPTLANSTHHNVRLLMLDDQRLLLPHWAKVVLTDPE 339

Qy        139 AAKYVHGIAVHWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AAKYVHGIAVHWYLDFLAPAKATLGETHRLFPNTMLFASEACVGSKFWEQSVRLGSWDRG 399

Qy        199 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 MQYSHSIITNLLYHVVGWTDWNLALNPEGGPNWVRNFVDSPIIVDITKDTFYKQPMFYHL 459

Qy        259 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSKDVPLTIKDPAVGFL 318
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GHFSKFIPEGSQRVGLVASQKNDLDAVALMHPDGSAVVVVLNRSSKDVPLTIKDPAVGFL 519

Qy        319 ETISPGYSIHTYLWHRQ 335
              |||||||||||||| ||
Db        520 ETISPGYSIHTYLWRRQ 536


RESULT 2
GLCM_PANTR
ID   GLCM_PANTR              Reviewed;         536 AA.
AC   Q9BDT0;
DT   21-NOV-2003, integrated into UniProtKB/Swiss-Prot.
DT   01-JUN-2001, sequence version 1.
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